

RHUS 20.1

10 20 30 40 50 60
 ATGAATAACA CATCTTGCAA CTTCAACGTC ACTCTAACG CATGGCACC AAGCCGATAC
 70 80 90 100 110 120
 ATAGCTATTG CTATGTACAG CATTGTTATC TGTATCGGGT TGGTTGGAAA CCTGCTGTTA
 130 140 150 160 170 180
 TGCATCGTGT TAGTCAAGAA ACGCAAACTG CGATATTCCA GCGATGTTA TTTTTTCCAC
 190 200 210 220 230 240
 GCCTCTATGG CCGACCTCGT CAGCACTGTC ATGCTACCGC TCTGGCTACA TTATGTCCTC
 250 260 270 280 290 300
 AACCTTGCCC AACTCTCTCG AGGAGCCTGT ATCAGCTTTT CGGTGACTTT CTATGTTCCC
 310 320 330 340 350 360
 CTTTCGTT AGGCCTGGTT ACTCATTTCC ATCGCTATGG AGCGATATTG CAACTTAGTA
 370 380 390 400 410 420
 TGGATGGCAC CCATTAGCGT TAAGACGGCC TTTAAACACT GCATAGGAAC CTGGATCGTA
 430 440 450 460 470 - 480
 TCTGCCCTCG TGGCATCACC CTACTACGCA TACAGAAACT CACACGACGA ACACGAATGC
 490 500 510 520 530 540
 ATTCTAGGAA ACTACACTTG GCACATTAAC GAACCGCTAC ACACGTGTAT GGATGTGGTG
 550 560 570 580 590 600
 ATCATAGTAT GGACCTTTT GGCCCCAGTA CTGGTAACCA TTATAGCAAG CGTCAAAATG
 610 620 630 640 650 660
 AGACGAACGA CCTGGGGCAA TACTAGGTTA AACGAAAAGA ACAGCGACAT TCTTATAGTA
 670 680 690 700 710 720
 CTAGTTGTCA TGACAGTGTGTT CTTTTGGGGA CCGTTTAATA TC GTGTTGGT TATTGACAAT
 730 740 750 760 770 780
 ATTTTACAGA GATACTATGA TACCACGAAT TGCGATGTAG AAAAGATTAA ACATATCATG
 790 800 810 820 830 840
 GCTATGATCT CAGAAGCCAT TGTTCATTTC CGCGGTATTA CAGCACCTAT TATTTATGTA
 850 860 870 880 890 900
 GGGATTAGTG GCAGATTTCG CGAAGAGATT TACTCTCTGT TTAGACGCCA GCCGTATAAC
 910 920 930 940 950 960
 GATTGGACC CCGATGCCAA TCAATTCAAT ATTGAACCTCA CTAGCCAGGG AAGAAGTAGA
 970 980 990 1000 1010 1020
 AATAGAAATG CTAGACAATC GGAAAGCAAT GTACCGCAAC CAGAAGAAATG CTTCTGGTAA
 1030 1040 1050 1060 1070 1080

FIG. 1

RHUS 28.2

10	20	30	40	50	60
ATGACCAACG CCGGACACTG TCACATAAAC GAAAGTCTCG CGTCGTATGG AATCGCTCCC					
70	80	90	100	110	120
GCAGCTACCA TTACCTTATA CAGCATTGCG GGAATCTGCG GTGTCACGGG AAATCTGTTA					
130	140	150	160	170	180
ATACTTTGG TTTTGTTCAC GAGACGCATA CACTGGTTCG CAAATGACAT CTACTATCTC					
190	200	210	220	230	240
AACATGATCT TTACAGACTT TCTTGTTTTC ATTACATTAC CCGCCTGGGT TTACTACCTG					
250	260	270	280	290	300
CTGAATTACA CACAACCTCTC ACACATATGCC TGCATTGCTC TATCATTTGT TTTTACGTT					
310	320	330	340	350	360
TCCATTTTA TTCAAGCTGA CTTTATGGTA GCAGTGGCTA TCGAGCGTTA TCGAAGCCTA					
370	380	390	400	410	420
GTGAAAAAAC AACCCTTAG CGTAAAAAAA GCCAGCGTCA GCTGCGCGTG CATCTGGATC					
430	440	450	460	470	480
ATTGTTATTA TAGTGTCTTC ACCATACTAC ATGTTAGAT CGCAACACGA AACAAATTCT					
490	500	510	520	530	540
TGCATTCTAG GAAACTACAC CTGGCATATG AACAGTCCTT TTCGCACAC AATGGACGCA					
550	560	570	580	590	600
TCCATTAACA TTTGGTCTTT TGTCGTTCCG GCCGTGACGA CCTTGTTAAT AGCCAGACGA					
610	620	630	640	650	660
ATTATATGTAT GTACTTCAGG CAACAAAAAA ATGAACGCCA GAGCCAGTGG TTTGTTAGAG					
670	680	690	700	710	720
GCCATGGTGA TTAGCATGTT ATTCTTCGGA GGACTTTCA ACCTGAACAT CTTCGAGAC					
730	740	750	760	770	780
ATAGTTTCGG ACACATCGGA AGACAATAAA GACTGCACAT ATCTTAAGCA GGAACACTTT					
790	800	810	820	830	840
ATTCGCATGG TCGGTGTGGC CCTCGTTAC GGGCGCGCTA TATTCAACCC TTTTATGTAT					
850	860	870	880	890	900
ATGTGTGTGA GTACCAGATT GCGCCAAGAA ATAAAATGTT TGTTTATGCG AATACCTTAT					
910	920	930	940	950	960
GAAACACTAG ATGCAGAACCA CGCTAAACTC ATGGTTAATT TAAAAAACAG AAATGCTAAT					
970	980	990	1000	1010	1020
GTACCCGATC CTAAACCTCG TGAATATGAA TCTGTGTTAT AG.....					

FIG. 2

RHUS 28.3

10	20	30	40	50	60
ATGACCAACA	CTAACAAATAC	GACTTGTCA	CTCAACGGAA	CTTTCGAAAC	TTTTAAAATC
70	80	90	100	110	120
ACCCGTCCAG	TAGCCATCA	CGCCTACACT	GTACTCGTGG	TTATCGGACT	TTTGGAAAC
130	140	150	160	170	180
ATTGTGCTGC	TCAGCGTGCT	CGTCGTGAA	CGCAAGCTCA	AGTTTCCGAA	TGACATTTAC
190	200	210	220	230	240
TTTTCAACG	CGTCTTGGC	AGACGTTTTT	GCCGTCTGCA	TGTTGCCCGC	CTGGGTTAAC
250	260	270	280	290	300
TATGCCACTGG	ACTCCACACCA	ACTTAGCAAG	TTCTCATGTA	TCACCTTTAC	GTTTGGTTT
310	320	330	340	350	360
TACGTCTCCC	TGTICATCCA	GGCCTGGATG	CTCATTCTGG	TCACCCCTGGA	GCGATAACGGA
370	380	390	400	410	420
TCTCTAGTCT	GGATCGCCCC	GATCACCAAGA	AACAAAGCCA	TAGCGAATTG	TGTACTCTT
430	440	450	460	470	480
TGGCTTGT	CCATCTTCTT	GGCCGCACCT	TACTACTCTT	TTAGAAACGA	AAGCAACGAA
490	500	510	520	530	540
CACCAATGCA	TCATGAGAAA	CTATAACCTGG	AGCGTTGGTG	AAACATGGCA	CATAGCCCTG
550	560	570	580	590	600
GATTCTTAA	TTACGCTCAT	TACATTATAC	ATGCCAGTGA	CTATTGTGTT	AGCTCTGAGT
610	620	630	640	650	660
TTCAAAATGG	CCAGATGGTC	AACCTTGGT	TACAGAAACC	TCACCAGCAG	AACCAGTCCT
670	680	690	700	710	720
ATCCTTATTT	TGATACTGAC	AGTAGCAGCA	GGGTCTGGG	GACCTTTCA	CCTATTTATG
730	740	750	760	770	780
TTTATAGAAA	ACGTGGCAGG	GCAGATTAC	CACATTAAA	AGGATTGCTG	GTACTTACAG
790	800	810	820	830	840
CTCAGACACT	TGTGTAGCTT	GATGACCGAA	ACCCTAGTGT	TTCTACGTTC	AGTTTTAAC
850	860	870	880	890	900
CCTTATATT	ATATGATAAT	CAGTTACAAG	TTTAGGCAGC	AGGTGCGCAG	TCTACTCAAG
910	920	930	940	950	960
CGTACTCAGT	ATGATGCTTT	GGACACGACT	CAGTTAGCAG	AAACTATGCA	GCTGAAAGCG
970	980	990	1000	1010	1020
AAAGGTGTG	CGGTGTCCGA	CCCCGCGCCG	CATGACTGCG	AATGCTTTT	GTAA.....

FIG. 3

Rhus 2B . 4

10 20 30 40 50 60
GAATTGAGC CAGCACACA TAAGCGTGT TCTCTCCATT GGAGCAGGGC CCGTCATTAC

70 80 90 100 110 120
CGGATACACG TGCCTTTTC TGTTGGGAT TCTGGGACAC TTTTACTTGT ATTGGAAAAA

130 140 150 160 170 180
CCATCAGAGA CGACACCGGA CAAACAGTTT CAGTGATGTT TTATTTGAC ATCTCATGAT

190 200 210 220 230 240
CACCGAAGAG GTCTTACCC TCACCATTCC CGTCTGGCG TATCACTTAA CTACTCACGG

250 260 270 280 290 300
CAAATTACCG GGCTCGTGGT GCCGAAGTCT CACCTTCGTT TTTTATCTAA CGGTATTGCG

310 320 330 340 350 360
TCGTGCCCTC TTTTACCTGC TCCTCATCTG GGACCGATAAC AGCGTAATCA TCTGCAGACA

370 380 390 400 410 420
CCCTCTCCCC GTTAATCTGA ACTACAGTCA GGTCA TAGGC CTGTCTGTCT GGCTGGTTGC

430 440 450 460 470 480
CGTACTGTCA GCATCACCGT TCTCCATTAA TAACGGAAGT GTGAAACAAT GCCTGGGCAA

490 500 510 520 530 540
CATGGGCAGC ATACCCAGCG AATCGTCTGC CGTTCTTAAC CTGGAAAGTGC ACCTGTGCTC

550 560 570 580 590 600
CTTCTGGTTA CCGCTCATCA TGTCGGCTAA CTGTTACTAC CAAGCAAAAC GCGGAGCATE

610 620 630 640 650 660
GCCTGACCAA CTCCACGAAC TTTACCGATG CAGTTGCTA ATTACCATTA TCACAACCTA

670 680 690 700 710 720
CGCTATCGTA TGGTTCCCTT TCCATCTCGC TTTACTCATA GACGCCCTGA TTAGCATAAG

730 740 750 760 770 780
CCATGTAGAA CCCTCTAGCG CTCTCCACTG GGCATCCATT GTCGTTACCT GTAAATCATT

790 800 810 820 830 840
TACATTTGTA TATGCGGGCA TAAGCCCAC AGTGTATTTC ACATGCTGCC CCACCGTACG

850 860 870 880 890 900
TCGGCGAAC TGATGTCTC TACGTCCATT CTTCACCTGG ATTTCCAGCA AAACCGGGCG

910 920 930 940 950 960
AGGCTACGCT CCGATTAACCA CACAACCTTT AAACATCCCC GACGAGCCGA TAGATAACAA

970 980 990 1000 1010 1020
GTCACCGCAC CTGTTAACG AATAA.....

FIG. 4

RHUS 28.5

10 20 30 40 50 60
 ATGACTACCA CCACAATGAG TGCTACCACG AATTCCAGTA CCACGCCCTCA AGCAAGCAGC
 70 80 90 100 110 120
 ACCACGATGA CAACGAAGAC AAGCACTCCT GGCAATACAA CTACTGGCAC TACGTCCACC
 130 140 150 160 170 180
 CTGACAACGA TATCAACAAAC TTCTAATGCT ACCAGCATAA CGTCTAATTAA AAGCACTACC
 190 200 210 220 230 240
 GGAAACCAAA CTGCAACTAC CAATGCTACT ACCTTCAGTT CCACATTAAC AACATCTACA
 250 260 270 280 290 300
 AATATAAGCA GTACATTTC GACAGTTCT ACCGTGCAT CCAATGCAAC ATGTAATTCT
 310 320 330 340 350 360
 ACAATCACAA CGAATATTAC AACTGCTTT ACTACAGCAG CAAACACTAC CGCAAGCAGC
 370 380 390 400 410 420
 CTCACCAGCA TCGTAACCTTC ACTTGCCACT ACCATTGAAA CCACATCATT TGATTATGAT
 430 440 450 460 470 480
 GAGTCAGCAG AAGCTTGCAA CTTAACAGAC ATCGTTCATCA CTACTAGATC AGTGACAGTT
 490 500 510 520 530 540
 ACTTTCTATA CTATCATATT CATACTCGGC CTTTTGGAA ACTTTCTGGT TCTTATGACC
 550 560 570 580 590 600
 ATCATTGGA ACCGTGCAT TTCCCTTATG GTTGAAATAT ATTCGTTAA TCTAGCAATC
 610 620 630 640 650 660
 TCCGATCTTA TGTTTGTATG TACTTTACCA TTTTGGATAA TGTATCTTCT TGAGCACGAC
 670 680 690 700 710 720
 GTCATGTCAC ATGCATCCTG TGTAGCAATG ACAGCCATT TTTATTGCGC GCTGTTGCC
 730 740 750 760 770 780
 AGCACTGTT TCCTCTTGCT AATTGTTTA GACAGATGTT ACGCTATTCT ATTAGGTACA
 790 800 810 820 830 840
 GAAAAAGCAA ATAGACGTT ATTGCGCAAT GCTGTTCTG GATGCATGCT CATGTGGGA
 850 860 870 880 890 900
 TTGTGTTCA TTTTAGCATT ACCTCATTAA ATCTTTATGA AGAAAGGAAC CAACGTATGT
 910 920 930 940 950 960
 GTAGCAGAGT ATGAACCAGG ACTTAACAAAT TTCTATGTTA TTTTATCAA TACTGAGGTG
 970 980 990 1000 1010 1020
 AACCTATGCA CCCTAGTTT GCCAGCCGCA GCCATTATCT ACTGGTATCT TAAACTAAC
 1030 1040 1050 1060 1070 1080
 AAAGCACTCA AAACCCATGA ACGACTGCGT CATAGGCTAA CGTCTCTAAA CATAGTGTAA
 1090 1100 1110 1120 1130 1140
 GCTGTTGTCA TTGTATTGTC TTTGTTTGG CTGCCGTATA ATCTCATGCT TATGATGTAT
 1150 1160 1170 1180 1190 1200
 AGCTTAGTTC ACATGCAGAT ACCTTGGGAA TGCAGCTCTG AAAAAATACT GAGACGAAGT
 1210 1220 1230 1240 1250 1260
 TTAATTATTA CAGAATCCAT CGCCCTCAGT CACTGTTGCA TCAACCCCAT TATCTACTTG

FIG. 5A

Rhus 28.5

1270 1280 1290 1300 1310 1320
CTCTTCGGAC CTCGCTGTG AAGCGAGTTC TGTCACTGT TGCATGTG CTTTACGCGC
1330 1340 1350 1360 1370 1380
TTATGTCCAC ACAGATCCTG GAGTTCCATA CGTGCAGAGA CGGTGTCCAT CAGTCTCAGT
1390 1400 1410 1420 1430 1440
CACTCACAGG TATCTGCATC ATCTGAGGAT GATGACAACG ATGTGCATGA TGAATTGCAA
1450 1460 1470 1480 1490 1500
TTTTTAATTT GA.....

FIG. 5B

RhUL33

10	20	30	40	50	60
ATGACCAATC TTTACTCTGC CAATTTCCTC ACCTTGATAG TACTTCCTTT TATCGTTTTA					
70	80	90	100	110	120
AGCAATCAAC ACCTTTTACC TGCCAGTGCA GTAACCTGTA AATTTCCTCTC CCTGTTGTAC					
130	140	150	160	170	180
TACTCTAGCT GCAGCGTAGG TTTGCTACA GTGGCACTGA TAGCGGCCGA CCGATACCGA					
190	200	210	220	230	240
GTGATTCACTC GCCGAACCTCA AGCTCGCCAA TCCTACCGTA ACACATATAT GATAGTAGGC					
250	260	270	280	290	300
TTAACGTGGC TCATTGGCTT GATCTGCGCT ACCCCCCGGG GGGTCTACAC AACCATIGTA					
310	320	330	340	350	360
GCTCACCGCG ATGGGGAAAG TGATGCTCAA AGACACAATA CTTCGATTAT GCACTTTGCG					
370	380	390	400	410	420
TATGATGAAG TTTACGTCCCT CATGGTCTGG AAACCTCTCA TCGTTTTAGT CTGGGGCATA					
430	440	450	460	470	480
GTGCCAGTTG TCATGATGAG CTGGTTTTAC GCGTTTTTT ACAATACTGT ACAAAAGAAC					
490	500	510	520	530	540
GCCAAAAAAC AACAAACGTAC GTTGAATTC GTAAAGGTAT TACTCCTGTC ATTCACTCATC					
550	560	570	580	590	600
ATCCAAACTC CCTATGTGTC AATCATGATT TTAAACACGT ATGCCACCGT AGGATGGCCG					
610	620	630	640	650	660
ATGGAATCCG CCGATCTAAC TAGACGCCGA GTCATCAACA CGTTTTCCCG TCTCGTCCCC					
670	680	690	700	710	720
AATCTACATT GCATGGTCAA CCCCATCCTC TACGCTCTCA TGGGAAATGA CTTTGTGTCT					
730	740	750	760	770	780
AAAGTGGGCC AATGCTTCG GGGGGAACTC ACGAACCGTC GAACTTTCT GCGTTCCAAG					
790	800	810	820	830	840
CAACAAGCCC GCAACTCGGA CGATGTACCG ACAATTGTCA GTCAACAACC CGCCACACCC					
850	860	870	880	890	900
ACCATCGTCA ATAAGCCCGA AAAAACCCG CACGTAAAAC GCGGTGTATC TTTCAGCGTC					
910	920	930	940	950	960
AGCGCATCTT CCGAACTCGC AGCGGCCAA AAAGCCAAAG ACAAAAGCCAA GCGGCTTTCC					
970	980	990	1000	1010	1020
ATGTCCCACC AAAACCTACG TCTGACGTGA					

FIG. 6

RhUL33 spliced

10 20 30 40 50 60
ATGGCAGTCA CTTTACGAGG CGGCAGCCCC ATAAAACTTTA AACTCATGAT TGTCAGCCAC

70 80 90 100 110 120
AGAAACCAGGA AATTTCACGA GATAACGGCTG TTTCAGCGTT CTGCTATCCG TCCAGGCGGG

130 140 150 160 170 180
TTATGGAAAC CATTCTTCAC AACCGAACG- -----

190 200 210 220 230 240
----- AGTGA AACTAATTCC

250 260 270 280 290 300
ATTTGCACA TCAACACCAC CTGCAATGTG ACCGACTCAC TGTACGCCGC CAAACTAGGC

310 320 330 340 350 360
GAAGCCCTCG TGAACAGCGC GCTAGCTTTA TTCGGTACCC CCCTCAACGC CATCGTCCTC

370 380 390 400 410 420
GTCACACAGC TATTGCCAA CCGAGTTCAT GGATACTCCA CCCCAGTTAT CTACATGACC

430 440 450 460 470 480
AATCTTTACT CTGCCAATT TCTCACCTTG ATAGTACTTC CTTTTATCGT TTTAAGCAAT

490 500 510 520 530 540
CAACACCTTT TACCTGCCAG TGCAGTAACC TGTAAATTTC TCTCCCTGTT GTACTACTCT

550 560 570 580 590 600
AGCTGCAGCG TAGGTTTTCG TACAGTGGCA CTGATAGCGG CCGACCGATA CCGAGTGATT

610 620 630 640 650 660
CATGCCGAA CTCAAGCTCG CCAATCCTAC CGTAACACAT ATATGATAGT AGGCTTAACG

670 680 690 700 710 720
TGGCTCATTG GCTTGATCTG CGCTACCCCC GGGGGGGTCT ACACAACCAT TGTAGCTCAC

730 740 750 760 770 780
CGCGATGGGG AAAGTGATGC TCAAAGACAC AATACTTGCA TTATGCACCT TGGGTATGAT

790 800 810 820 830 840
GAAGTTTACG TCCTCATGGT CTGGAAACTT CTCATCGTIT TAGTCIGGGG CATACTGCCA

850 860 870 880 890 900
GTTGTCATGA TGAGCTGGTT TTACGCGTTT TTTTACAATA CTGTACAAAG AACAGCCAAA

910 920 930 940 950 960
AAACAACAAAC GTACGTTGAA ATTCTGAAAG GTATTACTCC TGTCAATTCA CATCATCCAA

970 980 990 1000 1010 1020
ACTCCCTATG TGTCAATCAT GATTTTTAAC ACGTATGCCA CCGTAGGATG CCCGATGGAA

1030 1040 1050 1060 1070 1080
TGGCCCGATC TAACTAGACG CCGAGTCATC AACACGTTT CCCGTCTCGT CCCCAATCTA

1090 1100 1110 1120 1130 1140
CATIGCATGG TCAACCCCAT CCTCTACGCT CTCATGGAA ATGACTTTGT GTCTAAAGTG

1150 1160 1170 1180 1190 1200
GCCCAATGCT TTGGGGGGGA ACTCACGAAC CGTCGAACCT TTCTGCGTTC CAAGCAACAA

1210 1220 1230 1240 1250 1260
GCCCGCAACT CGGACGATGT ACCGACAATT GTCAGTCAAC AACCCGCCAC ACCCACCAC

RhUL33 spliced

1270	1280	1290	1300	1310	1320
GTCAATAAGC	CCGAAAAAAA	CCCGCACGTA	AAACGCGGTG	TATCTTCAG	CGTCAGCGCA
1330	1340	1350	1360	1370	1380
TCTTCCGAAC	TCGCAGCGGC	CAAAAAAGCC	AAAGACAAAG	CCAAGCGGCT	TTCCATGTCC
1390	1400	1410	1420	1430	1440
CACCAAAACC	TACGTCTGAC	GTGA.....

FIG. 7B

RHUL78

10	20	30	40	50	60
ATGATTACGG	AGCGCGTCCT	CGCAGGCATC	CTCGCGGGCA	TGACGGCCGC	GGGGAGTTTG
70	80	90	100	110	120
GTCATTCTCC	TCGCGGTTGT	TATGTGGTIG	AACATGTTAG	ATCGCGCTGG	CATGCCAATG
130	140	150	160	170	180
GCCGTTGGGC	ATTACACAGG	GAACCTGGTG	TTGACTCAGG	TCATCTGTAT	CTTCTCCATG
190	200	210	220	230	240
CTGGCGTCTA	AAATTGTTGG	CATGACGAGT	GC GGCCAACA	TGGGCTTCTG	CGGCATCGTG
250	260	270	280	290	300
GTTTTCTGG	AAGACACTGG	CCTCTATGTC	ACCTCGCTGC	TCTTCATGTT	TATGATCCTG
310	320	330	340	350	360
GATCGCATGG	CGGCTTTCT	TAACGGGCCT	CTTTCTGGA	GGCAGCAGAC	GACGAAGCAG
370	380	390	400	410	420
AATCTGAGTA	CAAGCGTGT	CATTATTCTG	TTTGCTGGG	TGTTGGGAAT	GGCCGCGGCT
430	440	450	460	470	480
GTTCCCAGCG	CGGCTGTGGC	TGCACCCAA	TCCAGGTGGG	AACGCTGCGA	AATTCCAGTG
490	500	510	520	530	540
TCATATGCCG	CAATCGACAT	GATTGTGAAG	CTCTGGTTTG	TGCTGTTGGC	ACCCGTCGTG
550	560	570	580	590	600
CTGATTATGG	CTGTGATCAT	TCAATCTTCC	TATCATCGTG	ATCGGGAGAG	GATCTGGTAC
610	620	630	640	650	660
TATGCCAGAC	GTGTGTTCAT	GTTCTACACG	GCCTGCTTTC	TCATGATGGT	GCCTTATTAC
670	680	690	700	710	720
TTCTCAGAG	TCATGCTGAG	CGACTTTGCT	TTGGTTGATA	TAAAAACAAA	AACGGCGAAC
730	740	750	760	770	780
AGCGACGGTT	GTGATTGAC	ATTCTTGAT	TATCTGAACA	TGTTCACTCA	CGTGATTAC
790	800	810	820	830	840
AGTTTTAAGT	TGGTGGTGTT	TGCTTTGTT	ATTGTCCTGT	TTTGCTCCAT	AAACCCGATG
850	860	870	880	890	900
GAAACGCTGG	AAGAATGCTT	GGAGAGGGCC	GATGCTGAGA	GGCAAAGTCG	GTCAGAAGCA
910	920	930	940	950	960
TCCCAGGGTG	AAAGGAGGCT	GCCAAATCAAC	ACATGCTGTA	TAAAGTTGAT	TGAATTGATA
970	980	990	1000	1010	1020
AAGCAGTATG	TAAGCACTCT	CTCTAAAGCC	ACGAGGGACA	ATTCTGGCGA	AAGGGCCAAT
1030	1040	1050	1060	1070	1080
TTGCCAGAGA	ATGCTGAAGA	TATTGGAACA	ACTGGCAGTG	ATCAGCTACC	GACTGAGGTC
1090	1100	1110	1120	1130	1140
ACCGTGACCC	CAATTCAATC	GGCTGTGTT	AGCACTGGAG	GAACGGTGTG	TCCAGTCTAA
1150	1160	1170	1180	1190	1200
.....